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RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/981,998A

DATE: 10/01/2001

TIME: 13:53:30

Input Set : A:\010910.revised.SUB.SEQUENCE.LST.0120.txt

Output Set: N:\CRF3\10012001\H981998A.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: PULST, STEFAN M.

8 (ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR  
9 ATAXIA-2 AND PRODUCTS RELATED THERETO

11 (iii) NUMBER OF SEQUENCES: 19

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.

15 (B) STREET: 119 NORTH FOURTH STREET, SUITE 203

16 (C) CITY: MINNEAPOLIS

17 (D) STATE: MINNESOTA

18 (E) COUNTRY: 55401

19 (F) ZIP: 55401

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/08/981,998A

C--> 29 (B) FILING DATE: 11-May-1998

30 (C) CLASSIFICATION:

44 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: WO 97/42314

34 (B) FILING DATE: 08-MAY-1997

37 (A) APPLICATION NUMBER: US 08/727,084

38 (B) FILING DATE: 08-OCT-1996

41 (A) APPLICATION NUMBER: US 60/022,207

42 (B) FILING DATE: 19-JUL-1996

45 (A) APPLICATION NUMBER: US 60/017,388

46 (B) FILING DATE: 08-MAY-1996

48 (viii) ATTORNEY/AGENT INFORMATION:

49 (A) NAME: MUETING, ANN M.

50 (B) REGISTRATION NUMBER: 33,977

51 (C) REFERENCE/DOCKET NUMBER: 232.00010120

53 (ix) TELECOMMUNICATION INFORMATION:

54 (A) TELEPHONE: 612-305-1217

55 (B) TELEFAX: 612-305-1228

58 (2) INFORMATION FOR SEQ ID NO: 1:

60 (i) SEQUENCE CHARACTERISTICS:

61 (A) LENGTH: 516 base pairs

62 (B) TYPE: nucleic acid

63 (C) STRANDEDNESS: both

64 (D) TOPOLOGY: both

66 (ii) MOLECULE TYPE: DNA (genomic)

71 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

73 TTGGTAGCAA CGGAAACGGC GGCGGCGCGT TTCGGCCCCG CTCCCGGCGG CTCCTTGCTC

60

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75 TCGGCGGGCC TCCCCGCCCC TTCGTCGTCG TCCTTCTCCC CCTCGCCAGC CCGGGCGCCC 120
77 CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCG TCGGTCCCCG CCGCGTTCCG 180
79 GCGTCTCCTT GGCGCGCCCG GCTCCCGGCT GTCCCCGCCC GGCGTGCGAG CCGGTGTATG 240
81 GGCCCTCAC CATGTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC 300
83 AGCAGCAACA GCAGCAGCAG CAGCAGCAGC AGCCGCCGCC CGCGGCTGCC AATGTCCGCA 360
85 AGCCCGGCGG CAGCGGCCTT CTAGCGTCGC CCGCCGCCGC GCCTTCGCCG TCCTCGTCTT 420
87 CCGTCTCCTC GTCCTCGGCC ACGGCTCCCT CCTCGGTGGT CGCGGCGACC TCCGGCGGCG 480
89 GGAGGCCCGG CCTGGGCAGG TGGGTGTCGG CACCCC 516

91 (2) INFORMATION FOR SEQ ID NO: 2:
93     (i) SEQUENCE CHARACTERISTICS:
94         (A) LENGTH: 4481 base pairs
95         (B) TYPE: nucleic acid
96         (C) STRANDEDNESS: both
97         (D) TOPOLOGY: both
99     (ii) MOLECULE TYPE: cDNA
102    (ix) FEATURE:
103        (A) NAME/KEY: CDS
104        (B) LOCATION: 163..4101
107    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
109 ACCCCCGAGA AAGCAACCCA GCGCGCCGCC CGCTCCTCAC GTGTCCCTCC CGGCCCCGGG 60
111 GCCACCTCAC GTTCTGCTTC CGTCTGACCC CTCCGACTTC CGGTAAAGAG TCCCTATCCG 120
113 CACCTCCGCT CCCACCCGGC GCCTCGGCGC GCCCGCCCTC CG ATG CGC TCA GCG 174
114                                     Met Arg Ser Ala
115                                     1
118 GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC TTC 222
119 Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg Phe
120 5 10 15 20
122 GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG CGG 270
123 Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala Arg
124 25 30 35
126 CGG AGC GGG CGG GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC TCC 318
127 Arg Ser Gly Arg Gly Gly Gly Ala Ala Pro Gly Pro Tyr Pro Ser
128 40 45 50
130 GCC GCC CCT CCC CCG CCC GGC CCC GGC CCC CCT CCC TCC CGG CAG AGC 366
131 Ala Ala Pro Pro Pro Gly Pro Gly Pro Pro Pro Ser Arg Gln Ser
132 55 60 65
134 TCG CCT CCC TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC GGC 414
135 Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn Gly Asn Gly Gly
136 70 75 80
138 GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGG CCT 462
139 Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly Leu Gly Gly Pro
140 85 90 95 100
142 CCC CGC CCC TTC GTC GTC GTC CTT CTC CCC CTC GCC AGC CCG GGC GCC 510
143 Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala Ser Pro Gly Ala
144 105 110 115
146 CCT CCG GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGT GCG TCC 558
147 Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly Ala Arg Ala Ser
148 120 125 130
150 CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT CCC 606

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151	Pro	Pro	Arg	Ser	Gly	Val	Ser	Leu	Ala	Arg	Pro	Ala	Pro	Gly	Cys	Pro	
152			135					140					145				
154	CGC	CCG	GCG	TGC	GAG	CCG	GTG	TAT	GGG	CCC	CTC	ACC	ATG	TCG	CTG	AAG	654
155	Arg	Pro	Ala	Cys	Glu	Pro	Val	Tyr	Gly	Pro	Leu	Thr	Met	Ser	Leu	Lys	
156		150					155					160					
158	CCC	CAG	CAG	CAG	CAG	CAG	CAG	CAG	CAA	CAG	CAG	CAG	CAG	CAA	CAG		702
159	Pro	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	
160	165					170					175					180	
162	CAG	CAG	CAG	CAG	CAG	CAG	CCG	CCG	CCC	GCG	GCT	GCC	AAT	GTC	CGC		750
163	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Pro	Pro	Ala	Ala	Ala	Asn	Val	Arg		
164				185					190					195			
166	AAG	CCC	GGC	GGC	AGC	GGC	CTT	CTA	GCG	TCG	CCC	GCC	GCC	GCG	CCT	TCG	798
167	Lys	Pro	Gly	Gly	Ser	Gly	Leu	Leu	Ala	Ser	Pro	Ala	Ala	Ala	Pro	Ser	
168			200						205				210				
170	CCG	TCC	TCG	TCC	TCG	GTC	TCC	TCG	TCC	TCG	GCC	ACG	GCT	CCC	TCC	TCG	846
171	Pro	Ser	Ser	Ser	Ser	Val	Ser	Ser	Ser	Ser	Ala	Thr	Ala	Pro	Ser	Ser	
172			215						220				225				
176	GTG	GTC	GCG	GCG	ACC	TCC	GGC	GGC	GGG	AGG	CCC	GGC	CTG	GGC	AGA	GGT	894
177	Val	Val	Ala	Ala	Thr	Ser	Gly	Gly	Gly	Arg	Pro	Gly	Leu	Gly	Arg	Gly	
178		230					235					240					
180	CGA	AAC	AGT	AAC	AAA	GGA	CTG	CCT	CAG	TCT	ACG	ATT	TCT	TTT	GAT	GGA	942
181	Arg	Asn	Ser	Asn	Lys	Gly	Leu	Pro	Gln	Ser	Thr	Ile	Ser	Phe	Asp	Gly	
182	245				250						255					260	
184	ATC	TAT	GCA	AAT	ATG	AGG	ATG	GTT	CAT	ATA	CTT	ACA	TCA	GTT	GTT	GGC	990
185	Ile	Tyr	Ala	Asn	Met	Arg	Met	Val	His	Ile	Leu	Thr	Ser	Val	Val	Gly	
186				265						270				275			
188	TCC	AAA	TGT	GAA	GTA	CAA	GTG	AAA	AAT	GGA	GGT	ATA	TAT	GAA	GGA	GTT	1038
189	Ser	Lys	Cys	Glu	Val	Gln	Val	Lys	Asn	Gly	Gly	Ile	Tyr	Glu	Gly	Val	
190			280						285					290			
192	TTT	AAA	ACT	TAC	AGT	CCG	AAG	TGT	GAT	TTG	GTA	CTT	GAT	GCC	GCA	CAT	1086
193	Phe	Lys	Thr	Tyr	Ser	Pro	Lys	Cys	Asp	Leu	Val	Leu	Asp	Ala	Ala	His	
194			295				300						305				
196	GAG	AAA	AGT	ACA	GAA	TCC	AGT	TCG	GGG	CCG	AAA	CGT	GAA	GAA	ATA	ATG	1134
197	Glu	Lys	Ser	Thr	Glu	Ser	Ser	Ser	Gly	Pro	Lys	Arg	Glu	Glu	Ile	Met	
198		310					315					320					
200	GAG	AGT	ATT	TTG	TTC	AAA	TGT	TCA	GAC	TTT	GTT	GTG	GTA	CAG	TTT	AAA	1182
201	Glu	Ser	Ile	Leu	Phe	Lys	Cys	Ser	Asp	Phe	Val	Val	Val	Gln	Phe	Lys	
202	325				330					335				340			
204	GAT	ATG	GAC	TCC	AGT	TAT	GCA	AAA	AGA	GAT	GCT	TTT	ACT	GAC	TCT	GCT	1230
205	Asp	Met	Asp	Ser	Ser	Tyr	Ala	Lys	Arg	Asp	Ala	Phe	Thr	Asp	Ser	Ala	
206				345						350				355			
208	ATC	AGT	GCT	AAA	GTG	AAT	GGC	GAA	CAC	AAA	GAG	AAG	GAC	CTG	GAG	CCC	1278
209	Ile	Ser	Ala	Lys	Val	Asn	Gly	Glu	His	Lys	Glu	Lys	Asp	Leu	Glu	Pro	
210			360						365				370				
212	TGG	GAT	GCA	GGT	GAA	CTC	ACA	GCC	AAT	GAG	GAA	CTT	GAG	GCT	TTG	GAA	1326
213	Trp	Asp	Ala	Gly	Glu	Leu	Thr	Ala	Asn	Glu	Glu	Leu	Glu	Ala	Leu	Glu	
214			375					380				385					
216	AAT	GAC	GTA	TCT	AAT	GGA	TGG	GAT	CCC	AAT	GAT	ATG	TTT	CGA	TAT	AAT	1374
217	Asn	Asp	Val	Ser	Asn	Gly	Trp	Asp	Pro	Asn	Asp	Met	Phe	Arg	Tyr	Asn	

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218	390	395	400	
220	GAA GAA AAT TAT GGT GTA GTG TCT ACG TAT GAT AGC AGT TTA TCT TCG	1422		
221	Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser			
222	405 410 415 420			
224	TAT ACA GTG CCC TTA GAA AGA GAT AAC TCA GAA GAA TTT TTA AAA CGG	1470		
225	Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg			
226	425 430 435			
228	GAA GCA AGG GCA AAC CAG TTA GCA GAA GAA ATT GAG TCA AGT GCC CAG	1518		
229	Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln			
230	440 445 450			
234	TAC AAA GCT CGA GTG GCC CTG GAA AAT GAT GAT AGG AGT GAG GAA GAA	1566		
235	Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu			
236	455 460 465			
238	AAA TAC ACA GCA GTT CAG AGA AAT TCC AGT GAA CGT GAG GGG CAC AGC	1614		
239	Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg Glu Gly His Ser			
240	470 475 480			
242	ATA AAC ACT AGG GAA AAT AAA TAT ATT CCT CCT GGA CAA AGA AAT AGA	1662		
243	Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg			
244	485 490 495 500			
246	GAA GTC ATA TCC TGG GGA AGT GGG AGA CAG AAT TCA CCG CGT ATG GGC	1710		
247	Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser Pro Arg Met Gly			
248	505 510 515			
250	CAG CCT GGA TCG GGC TCC ATG CCA TCA AGA TCC ACT TCT CAC ACT TCA	1758		
251	Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr Ser His Thr Ser			
252	520 525 530			
254	GAT TTC AAC CCG AAT TCT GGT TCA GAC CAA AGA GTA GTT AAT GGA GGT	1806		
255	Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val Val Asn Gly Gly			
256	535 540 545			
258	GTT CCC TGG CCA TCG CCT TGC CCA TCT CCT TCC TCT CGC CCA CCT TCT	1854		
259	Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser Arg Pro Pro Ser			
260	550 555 560			
262	CGC TAC CAG TCA GGT CCC AAC TCT CTT CCA CCT CGG GCA GCC ACC CCT	1902		
263	Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg Ala Ala Thr Pro			
264	565 570 575 580			
266	ACA CGG CCG CCC TCC AGG CCC CCC TCG CGG CCA TCC AGA CCC CCG TCT	1950		
267	Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser Arg Pro Pro Ser			
268	585 590 595			
270	CAC CCC TCT GCT CAT GGT TCT CCA GCT CCT GTC TCT ACT ATG CCT AAA	1998		
271	His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser Thr Met Pro Lys			
272	600 605 610			
274	CGC ATG TCT TCA GAA GGG CCT CCA AGG ATG TCC CCA AAG GCC CAG CGA	2046		
275	Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro Lys Ala Gln Arg			
276	615 620 625			
278	CAT CCT CGA AAT CAC AGA GTT TCT GCT GGG AGG GGT TCC ATA TCC AGT	2094		
279	His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly Ser Ile Ser Ser			
280	630 635 640			
282	GGC CTA GAA TTT GTA TCC CAC AAC CCA CCC AGT GAA GCA GCT ACT CCT	2142		
283	Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu Ala Ala Thr Pro			
284	645 650 655 660			

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286	CCA	GTA	GCA	AGG	ACC	AGT	CCC	TCG	GGG	GGA	ACG	TGG	TCA	TCA	GTG	GTC	2190
287	Pro	Val	Ala	Arg	Thr	Ser	Pro	Ser	Gly	Gly	Thr	Trp	Ser	Ser	Val	Val	
288				665					670						675		
292	AGT	GGG	GTT	CCA	AGA	TTA	TCC	CCT	AAA	ACT	CAT	AGA	CCC	AGG	TCT	CCC	2238
293	Ser	Gly	Val	Pro	Arg	Leu	Ser	Pro	Lys	Thr	His	Arg	Pro	Arg	Ser	Pro	
294				680					685						690		
296	AGA	CAG	AAC	AGT	ATT	GGA	AAT	ACC	CCC	AGT	GGG	CCA	GTT	CTT	GCT	TCT	2286
297	Arg	Gln	Asn	Ser	Ile	Gly	Asn	Thr	Pro	Ser	Gly	Pro	Val	Leu	Ala	Ser	
298				695				700					705				
300	CCC	CAA	GCT	GGT	ATT	ATT	CCA	ACT	GAA	GCT	GTT	GCC	ATG	CCT	ATT	CCA	2334
301	Pro	Gln	Ala	Gly	Ile	Ile	Pro	Thr	Glu	Ala	Val	Ala	Met	Pro	Ile	Pro	
302		710					715					720					
304	GCT	GCA	TCT	CCT	ACG	CCT	GCT	AGT	CCT	GCA	TCG	AAC	AGA	GCT	GTT	ACC	2382
305	Ala	Ala	Ser	Pro	Thr	Pro	Ala	Ser	Pro	Ala	Ser	Asn	Arg	Ala	Val	Thr	
306	725					730				735					740		
308	CCT	TCT	AGT	GAG	GCT	AAA	GAT	TCC	AGG	CTT	CAA	GAT	CAG	AGG	CAG	AAC	2430
309	Pro	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Arg	Leu	Gln	Asp	Gln	Arg	Gln	Asn	
310				745					750						755		
312	TCT	CCT	GCA	GGG	AAT	AAA	GAA	AAT	ATT	AAA	CCC	AAT	GAA	ACA	TCA	CCT	2478
313	Ser	Pro	Ala	Gly	Asn	Lys	Glu	Asn	Ile	Lys	Pro	Asn	Glu	Thr	Ser	Pro	
314				760					765				770				
316	AGC	TTC	TCA	AAA	GCT	GAA	AAC	AAA	GGT	ATA	TCA	CCA	GTT	GTT	TCT	GAA	2526
317	Ser	Phe	Ser	Lys	Ala	Glu	Asn	Lys	Gly	Ile	Ser	Pro	Val	Val	Ser	Glu	
318				775				780					785				
320	CAT	AGA	AAA	CAG	ATT	GAT	GAT	TTA	AAG	AAA	TTT	AAG	AAT	GAT	TTT	AGG	2574
321	His	Arg	Lys	Gln	Ile	Asp	Asp	Leu	Lys	Lys	Phe	Lys	Asn	Asp	Phe	Arg	
322		790					795					800					
324	TTA	CAG	CCA	AGT	TCT	ACT	TCT	GAA	TCT	ATG	GAT	CAA	CTA	CTA	AAC	AAA	2622
325	Leu	Gln	Pro	Ser	Ser	Thr	Ser	Glu	Ser	Met	Asp	Gln	Leu	Leu	Asn	Lys	
326	805					810				815					820		
328	AAT	AGA	GAG	GGA	GAA	AAA	TCA	AGA	GAT	TTG	ATC	AAA	GAC	AAA	ATT	GAA	2670
329	Asn	Arg	Glu	Gly	Glu	Lys	Ser	Arg	Asp	Leu	Ile	Lys	Asp	Lys	Ile	Glu	
330				825					830						835		
332	CCA	AGT	GCT	AAG	GAT	TCT	TTC	ATT	GAA	AAT	AGC	AGC	AGC	AAC	TGT	ACC	2718
333	Pro	Ser	Ala	Lys	Asp	Ser	Phe	Ile	Glu	Asn	Ser	Ser	Ser	Asn	Cys	Thr	
334				840					845					850			
336	AGT	GGC	AGC	AGC	AAG	CCG	AAT	AGC	CCC	AGC	ATT	TCC	CCT	TCA	ATA	CTT	2766
337	Ser	Gly	Ser	Ser	Lys	Pro	Asn	Ser	Pro	Ser	Ile	Ser	Pro	Ser	Ile	Leu	
338				855				860					865				
340	AGT	AAC	ACG	GAG	CAC	AAG	AGG	GGA	CCT	GAG	GTC	ACT	TCC	CAA	GGG	GTT	2814
341	Ser	Asn	Thr	Glu	His	Lys	Arg	Gly	Pro	Glu	Val	Thr	Ser	Gln	Gly	Val	
342		870					875					880					
344	CAG	ACT	TCC	AGC	CCA	GCA	TGT	AAA	CAA	GAG	AAA	GAC	GAT	AAG	GAA	GAG	2862
345	Gln	Thr	Ser	Ser	Pro	Ala	Cys	Lys	Gln	Glu	Lys	Asp	Asp	Lys	Glu	Glu	
346	885					890				895					900		
350	AAG	AAA	GAC	GCA	GCT	GAG	CAA	GTT	AGG	AAA	TCA	ACA	TTG	AAT	CCC	AAT	2910
351	Lys	Lys	Asp	Ala	Ala	Glu	Gln	Val	Arg	Lys	Ser	Thr	Leu	Asn	Pro	Asn	
352				905					910						915		
354	GCA	AAG	GAG	TTC	AAC	CCA	CGT	TCC	TTC	TCT	CAG	CCA	AAG	CCT	TCT	ACT	2958

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]